

## SEQUENCE LISTING

<110> Reinhard Ebner  
Steven M. Ruben

<120> INTERLEUKINS-21 AND 22

<130> PF470

<140> Unknown

<141> 1999-05-27

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<151> 1998-05-29

<150> 60/099,805  
<151> 1998-09-10

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<170> PatentIn Ver. 2.0

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Ala Glu Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu  
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aca gct gcg ctc aac tcc gtg cgg ctg ctc cag agc ctg ctg gtg ctg 145  
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cgc cgc cgg ccc tgc tcc cgc gac ggc tcg ggg ctc ccc aca cct ggg 193  
Arg Arg Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly  
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gcc ttt gcc ttc cac acc gag ttc atc cac gtc ccc gtc ggc tgc acc 241  
Ala Phe Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr  
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tgc gtg ctg ccc cgt tca gtg tgaccgccaa ggccgtgggg cccttagact 292  
Cys Val Leu Pro Arg Ser Val  
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cctcccccaa cactaccctt ggggtctggg cattccccgt gtctggagga cagcccccca 412

ctgttctcct catctccagc ctcagtagtt ggggtwgaa ggagctcagc acctcttcca 472  
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 Leu Gln Leu Gly Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala  
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 ggg ggc agg ccc gcc gac cgc cgc ttc ccg ccg ccc acc aac ctg cgc 143  
 Gly Gly Arg Pro Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg  
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 Ser Val Ser Pro Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr  
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 Val Ser Pro Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro  
 50 55 60  
 Arg Tyr Leu Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly  
 65 70 75 80  
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 85 90 95  
 Pro Thr Val Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser  
 100 105 110  
 Val Tyr Thr Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys Val  
 115 120 125  
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 35 40 45  
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 Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu  
 65 70 75 80  
 Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His  
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Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser  
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Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His  
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 35 40 45

Val Asn Leu Lys Val Phe Asn Ser Leu Gly Ala Lys Val Ser Ser Arg  
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Arg Pro Ser Asp Tyr Leu Asn Arg Ser Thr Ser Pro Trp Thr Leu His  
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Cys Arg His Gln Arg Cys Val Asn Ala Glu Gly Lys Leu Asp His His  
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Arg Ser Thr Ser Pro Trp Thr Leu His Arg Asn Glu Asp Gln Asp Arg  
 65 70 75 80

Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg Tyr Leu Gly Cys Val  
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Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln  
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Gln Glu Ile Leu Val Val Arg Lys Gly His Gln Pro Cys Pro Asn Ser  
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Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala  
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Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg  
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Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile  
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Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn  
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tcaagttcaa ctggtaacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240  
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300  
ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccatcg 360  
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 cagttccgccc cattctccgc cccatggctg actaattttt tttatattatg cagaggccga 180  
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ttgaatagag gcagagctta ttttatatta tccaaatgag agctactctg ttnacattt 300  
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ctgccccggg aggtctcccc ggncccgcat cccgaggcgc ccaagctgga gccgcctgga 180  
ggnttcggtc ggcgactctg aagagagtnc accgagcaaa ccaagtgccg gagcaacagc 240  
gncgnctttt ncatggagat tcgtaagcan ttttcatttg acangggat ccctggtttgc 300  
tttttagtta caagcaagca nntggnttga agtnngntggg gaaaggancc gnagggattc 360  
tgtnttnggg gccntntgga gggttttgga aaatttnagg gggtnctgn gggttttta 420  
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gcagaaacag aagccnccag atnganctcn gcagatgcta acgnggccc 178

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gggcttcgggt ncggcgaacc tctgaaagag aagtgccacc gagcaaacca agtgcggta 180

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 35 40 45  
 Pro His Leu Leu Ala Arg Gly Ala Lys Trp Gly Gln Ala Leu Pro Val  
 50 55 60  
 Ala Leu Val Ser Ser Leu Glu Ala Ala Ser His Arg Gly Arg His Glu  
 65 70 75 80  
 Arg Pro Ser Ala Thr Thr Gln Cys Pro Val Leu Arg Pro Glu Glu Val  
 85 90 95  
 Leu Glu Ala Asp Thr His Gln Arg Ser Ile Ser Pro Trp Arg Tyr Arg  
 100 105 110  
 Val Asp Thr Asp Glu Asp Arg Tyr Pro Gln Lys Leu Ala Phe Ala Glu  
 115 120 125  
 Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu Thr Ala  
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 Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu Arg Arg  
 145 150 155 160  
 Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly Ala Phe  
 165 170 175  
 Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr Cys Val  
 180 185 190  
 Leu Pro Arg Ser Val  
 195

<210> 30  
 <211> 332  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
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 <222> (162)  
 <223> n equals a, t, g or c  
 <220>  
 <221> misc\_feature

<222> (194)  
<223> n equals a, t, g or c

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<220>
<221> misc_feature
<222> (214)
<223> n equals a, t, g or c
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<220>
<221> misc_feature
<222> (260)
<223> n equals a, t, g or c
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<220>
<221> misc_feature
<222> (277)
<223> n equals a, t, q or c
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<220>
<221> misc_feature
<222> (290)
<223> n equals a, t, q or c
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<220>
<221> misc_feature
<222> (305)
<223> n equals a, t, q or c
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<220>
<221> misc_feature
<222> (314)
<223> n equals a, t, q or c
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<400> 30
tggacacgta tgaggaccgc tatccacaga agctggcctt cgccgagtgc ctgtgcagag 60
gctgtatcga tgcacggacg ggccgcgaga cagctgcgtc caactccgtg cggctgctcc 120
agagcctgac tggtgctgcg ccgccccccc tgactacccg cnacggacta cgggggctac 180
cccacacctg gggncctttg accttccaca ccgnagttac atgccacgta ccccgttcgg 240
gctgtcacct gacgtgctgn ccccgtttac agtgtgnacc gaccgttaggn ccgtggggtc 300
ccctnagtagtac tgggnacacgt gtgatacccc ag 332
```

<210> 31  
<211> 522  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> CDS  
<222> (1) .. (522)

<400> 31  
ggc tgc gcg gac cgg ccg gag gag cta ctg gag cag ctg tac ggg cgc 48  
Gly Cys Ala Asp Arg Pro Glu Glu Leu Leu Glu Gln Leu Tyr Gly Arg  
1 5 10 15

ctg gcg gcc ggc gtg ctc agt gcc ttc cac cac acg ctg cag ctg ggg 96  
 Leu Ala Ala Gly Val Leu Ser Ala Phe His His Thr Leu Gln Leu Gly

	20	25	30	
ccg cgt gag cag gcg cgc aac ggc agc tgc ccg gca ggg ggc agg ccc Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro	35	40	45	144
gcc gac cgc cgc ttc cgg ccc acc aac ctg cgc agc gtg tcg ccc Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser Val Ser Pro	50	55	60	192
tgg gcc tac aga atc tcc tac gac ccg gcg agg tac ccc agg tac ctg Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu	65	70	75	240
cct gaa gcc tac tgc ctg tgc cgg ggc tgc ctg acc ggg ctg ttc ggc Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly	85	90	95	288
gag gag gac gtg cgc ttc cgc agc gcc cct gtc tac atg ccc acc gtc Glu Glu Asp Val Arg Phe Arg Ser Ala Pro Val Tyr Met Pro Thr Val	100	105	110	336
gtc ctg cgc cgc acc ccc gcc tgc gcc ggc cgt tcc gtc tac acc Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr	115	120	125	384
gag gcc tac gtc acc atc ccc gtg ggc tgc acc tgc gtc ccc gag ccg Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys Val Pro Glu Pro	130	135	140	432
gag aag gac gca gac agc atc aac tcc agc atc gac aaa cag ggc gcc Glu Lys Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys Gln Gly Ala	145	150	155	480
aag ctc ctg ctg ggc ccc aac gac gcg ccc gct ggc ccc tga Lys Leu Leu Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro	165	170		522

<210> 32  
<211> 173  
<212> PRT  
<213> Homo sapiens

<400> 32				
Gly Cys Ala Asp Arg Pro Glu Glu Leu Leu Glu Gln Leu Tyr Gly Arg	1	5	10	15
Leu Ala Ala Gly Val Leu Ser Ala Phe His His Thr Leu Gln Leu Gly	20	25	30	
Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro	35	40	45	
Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser Val Ser Pro	50	55	60	
Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu	65	70	75	80
Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly	85	90	95	

Glu Glu Asp Val Arg Phe Arg Ser Ala Pro Val Tyr Met Pro Thr Val  
100 105 110

Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr  
115 120 125

Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys Val Pro Glu Pro  
130 135 140

Glu Lys Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys Gln Gly Ala  
145 150 155 160

Lys Leu Leu Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro  
165 170